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P#S 1600

RAW SEQUENCE LISTING

DATE: 04/25/2002

PATENT APPLICATION: US/09/573,630A

TIME: 09:10:09

Input Set : A:\Pto.amc

Output Set: N:\CRF3\04252002\I573630A.raw

ENTERED

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3 <110> APPLICANT: MERCHANT, JUANITA L.
5 <120> TITLE OF INVENTION: ACINETOBACTER OUTER MEMBRANE PROTEIN AND GENE SEQUENCE
6   COMPOSITIONS AND METHODS
8 <130> FILE REFERENCE: 4100.001700
10 <140> CURRENT APPLICATION NUMBER: 09/573,630A
11 <141> CURRENT FILING DATE: 2000-05-17
13 <150> PRIOR APPLICATION NUMBER: 60/134,399
14 <151> PRIOR FILING DATE: 1999-05-17
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1050
22 <212> TYPE: DNA
23 <213> ORGANISM: Acinetobacter sp.
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26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1047)
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31 Met Lys Met Ser Arg Ile Ala Leu Ala Met Leu Val Ala Ala Pro Phe
32   1               5               10              15
34 gct gct gca aat gca ggc gta act gtt act ccg ttg atg ttg ggg tac      96
35 Ala Ala Ala Asn Ala Gly Val Thr Val Thr Pro Leu Met Leu Gly Tyr
36           20               25              30
38 act ttt caa gat acc cag cat aac aat aac ggt aat gat ggc gaa ctt      144
39 Thr Phe Gln Asp Thr Gln His Asn Asn Asn Gly Asn Asp Gly Glu Leu
40           35               40              45
42 act agt agt cct gaa tta caa gac gat tta ttc gta ggt gct gct att      192
43 Thr Ser Ser Pro Glu Leu Gln Asp Asp Leu Phe Val Gly Ala Ala Ile
44           50               55              60
46 ggt gtt gaa tta act cct tgg tta ggt ttt gaa gct gaa tat agc caa      240
47 Gly Val Glu Leu Thr Pro Trp Leu Gly Phe Glu Ala Glu Tyr Ser Gln
48   65               70              75              80
50 gta aag ggc gat gtt gac ggt gct gct gaa ggt gca gaa tac aaa ggc      288
51 Val Lys Gly Asp Val Asp Gly Ala Ala Glu Gly Ala Glu Tyr Lys Gly
52           85               90              95
54 caa aat att gca ggt aac ttc tac gca act tct gac gta ttt act ggt      336
55 Gln Asn Ile Ala Gly Asn Phe Tyr Ala Thr Ser Asp Val Phe Thr Gly
56           100              105             110
58 aac tat gac agc aaa gtg aag cca tat atg ctt cta ggt gcg ggt cac      384
59 Asn Tyr Asp Ser Lys Val Lys Pro Tyr Met Leu Leu Gly Ala Gly His
60           115              120             125
62 tac aaa tac gaa ttt gaa ggt gtg cca cgc ggt act cgc ggt aat gaa      432

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63 Tyr Lys Tyr Glu Phe Glu Gly Val Pro Arg Gly Thr Arg Gly Asn Glu
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66 gaa gaa ggt act cta ggt aat gct ggt gtg ggt gca ttc tgg cac atc 480
67 Glu Glu Gly Thr Leu Gly Asn Ala Gly Val Gly Ala Phe Trp His Ile
68 145      150      155      160
70 aac gat gcc tta gcg cta cgt act gaa gct cgt ggt act tac cac ttt 528
71 Asn Asp Ala Leu Ala Leu Arg Thr Glu Ala Arg Gly Thr Tyr His Phe
72      165      170      175
74 gac gaa aaa ttc tgg aac tac aca gca tta gct ggt ctt aat gtt gtt 576
75 Asp Glu Lys Phe Trp Asn Tyr Thr Ala Leu Ala Gly Leu Asn Val Val
76      180      185      190
78 cta ggt ggt cgt ctg aaa cca gct gct cca gta gtt gaa gtt gct cca 624
79 Leu Gly Gly Arg Leu Lys Pro Ala Ala Pro Val Val Glu Val Ala Pro
80      195      200      205
82 gtt gag cct gta act cca gtt gct cca ccg cca caa gag ttg act gaa 672
83 Val Glu Pro Val Thr Pro Val Ala Pro Pro Pro Gln Glu Leu Thr Glu
84      210      215      220
86 gac ctg aac atg gaa ctt cgt gtt ttt ttc gac act aac aaa agc aac 720
87 Asp Leu Asn Met Glu Leu Arg Val Phe Phe Asp Thr Asn Lys Ser Asn
88 225      230      235      240
90 atc aaa gat caa tac aaa cca gaa atc gct aaa gtt gct gag aag cta 768
91 Ile Lys Asp Gln Tyr Lys Pro Glu Ile Ala Lys Val Ala Glu Lys Leu
92      245      250      255
94 gtt gaa tat cca aac gct act gct cgt atc gaa ggt cac act gac aac 816
95 Val Glu Tyr Pro Asn Ala Thr Ala Arg Ile Glu Gly His Thr Asp Asn
96      260      265      270
98 act ggt cca cgt gca cta aac gaa cgt tta tct cta gca cgt gct aac 864
99 Thr Gly Pro Arg Ala Leu Asn Glu Arg Leu Ser Leu Ala Arg Ala Asn
100      275      280      285
102 tct gtt aaa tct tcg ctt gta aat gaa tac aat gtt gat gca tct cgc 912
103 Ser Val Lys Ser Ser Leu Val Asn Glu Tyr Asn Val Asp Ala Ser Arg
104      290      295      300
106 ttg tct act caa ggt ttc gct tgg gat caa ccg att gct gac aac aac 960
107 Leu Ser Thr Gln Gly Phe Ala Trp Asp Gln Pro Ile Ala Asp Asn Asn
108 305      310      315      320
110 act aaa gaa ggt cgt gct atg aac cgt cgt gta ttc gcg aca atc act 1008
111 Thr Lys Glu Gly Arg Ala Met Asn Arg Arg Val Phe Ala Thr Ile Thr
112      325      330      335
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122 <213> ORGANISM: Acinetobacter sp.
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131 Thr Phe Gln Asp Thr Gln His Asn Asn Asn Gly Asn Asp Gly Glu Leu
132          35          40          45
134 Thr Ser Ser Pro Glu Leu Gln Asp Asp Leu Phe Val Gly Ala Ala Ile
135          50          55          60
137 Gly Val Glu Leu Thr Pro Trp Leu Gly Phe Glu Ala Glu Tyr Ser Gln
138 65          70          75          80
140 Val Lys Gly Asp Val Asp Gly Ala Ala Glu Gly Ala Glu Tyr Lys Gly
141          85          90          95
143 Gln Asn Ile Ala Gly Asn Phe Tyr Ala Thr Ser Asp Val Phe Thr Gly
144          100          105          110
146 Asn Tyr Asp Ser Lys Val Lys Pro Tyr Met Leu Leu Gly Ala Gly His
147          115          120          125
149 Tyr Lys Tyr Glu Phe Glu Gly Val Pro Arg Gly Thr Arg Gly Asn Glu
150          130          135          140
152 Glu Glu Gly Thr Leu Gly Asn Ala Gly Val Gly Ala Phe Trp His Ile
153 145          150          155          160
155 Asn Asp Ala Leu Ala Leu Arg Thr Glu Ala Arg Gly Thr Tyr His Phe
156          165          170          175
158 Asp Glu Lys Phe Trp Asn Tyr Thr Ala Leu Ala Gly Leu Asn Val Val
159          180          185          190
161 Leu Gly Gly Arg Leu Lys Pro Ala Ala Pro Val Val Glu Val Ala Pro
162          195          200          205
164 Val Glu Pro Val Thr Pro Val Ala Pro Pro Pro Gln Glu Leu Thr Glu
165          210          215          220
167 Asp Leu Asn Met Glu Leu Arg Val Phe Phe Asp Thr Asn Lys Ser Asn
168 225          230          235          240
170 Ile Lys Asp Gln Tyr Lys Pro Glu Ile Ala Lys Val Ala Glu Lys Leu
171          245          250          255
173 Val Glu Tyr Pro Asn Ala Thr Ala Arg Ile Glu Gly His Thr Asp Asn
174          260          265          270
176 Thr Gly Pro Arg Ala Leu Asn Glu Arg Leu Ser Leu Ala Arg Ala Asn
177          275          280          285
179 Ser Val Lys Ser Ser Leu Val Asn Glu Tyr Asn Val Asp Ala Ser Arg
180          290          295          300
182 Leu Ser Thr Gln Gly Phe Ala Trp Asp Gln Pro Ile Ala Asp Asn Asn
183 305          310          315          320
185 Thr Lys Glu Gly Arg Ala Met Asn Arg Arg Val Phe Ala Thr Ile Thr
186          325          330          335
188 Gly Ser Arg Thr Val Leu Ala Glu Gln Pro Val Ala Gln
189          340          345
193 <210> SEQ ID NO: 3
194 <211> LENGTH: 36
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
200 OLIGONUCLEOTIDE
202 <400> SEQUENCE: 3

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207 <211> LENGTH: 39
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
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215 <400> SEQUENCE: 4
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219 <210> SEQ ID NO: 5
220 <211> LENGTH: 36
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
226 OLIGONUCLEOTIDE
228 <400> SEQUENCE: 5
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232 <210> SEQ ID NO: 6
233 <211> LENGTH: 1701
234 <212> TYPE: DNA
235 <213> ORGANISM: Acinetobacter sp.
237 <400> SEQUENCE: 6
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240 accggccccc cttcgagttc gacggtatcg ataagcttga tatcgaatta actcaacaat 180
241 agtgaatgct cttgttattt ttttatacat agagttacct gatttatata ttatttttat 240
242 gaggaatatg ttattaatta tgcgtttttt atgctttgtg gagccgagta atcagtcctt 300
243 acttaagttt caagaaagtg attaaaaaat aattggcaat caccataggg tattcagaat 360
244 aaaaaattga gtaaaaagtt accgaattac aacggaaatt gtaagtaatt ttgtcaataa 420
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246 gtgaatagct taagaataaa actggggtaa taaaaagcct atctcaggat ggcctattgc 540
247 gggcttgagc ttgaacaaca atttttatct ctggaggata aatccatgaa aatgagtcgt 600
248 attgctttag ctatgcttgt agctgcacct tttgctgctg caaatgcagg cgtaactgtt 660
249 actccgttga tgttggggta cacttttcaa gatacccagc ataacaataa cggtaatgat 720
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261 atcgaaggtc acactgacaa cactggtcca cgtgcactaa acgaacgttt atctctagca 1440
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264 gctatgaacc gtcgtgtatt cgcgacaatc actggtagcc gtactgtttt agctgaacaa 1620
265 ccagttgctc aataattcat tattgaacac tcattaaaag gcagctcttc gacctgcttt 1680
266 tttagtctgt atttgactac c                                     1701
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VERIFICATION SUMMARY

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